



SEQUENCE LISTING

<110> Rosey, Everett L.
Strugnell, Richard A.
Good, Robert T,
King, Kendall W.

<120> NOVEL THERAPEUTIC COMPOSITIONS FOR
TREATING INFECTION BY LAWSONIA SPP.

<130> DAVI110.001AUS

<140> US 10/010,160
<141> 2001-11-09

<150> AU PR1381
<151> 2000-11-10

<150> US 60/249,596
<151> 2000-11-17

<160> 68

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Lawsonia intracellularis

<220>
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<222> (1)...(621)

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1 5 10 15

cag gaa gct cgt tct gaa ggg agt gtc cct aaa tca gaa gag gtt act 96
Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr
20 25 30

aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca 144
Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
35 40 45

ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca 192
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
50 55 60

gaa tca ttt cgg ttt gag gtt aca gca cag tca gta tat gct tta ttt 240
Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe

65	70	75	80	
att tat gtt gct caa gag ata got att tta ttg atg cca ata tta ctt				288
Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu				
85	90	95		
ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca				336
Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala				
100	105	110		
tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata				384
Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile				
115	120	125		
ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga				432
Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg				
130	135	140		
ctt tta cgt agt tta gtt caa gta att gtt ata ggt att gtt cca tat				480
Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr				
145	150	155	160	
atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca				528
Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala				
165	170	175		
agt cct tca ggt gtg gca gat tat atg ctt aat aca gga ata gta ctt				576
Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu				
180	185	190		
gtt tta tat acg cta att cct atg aca att att gca gtc gca gat				621
Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp				
195	200	205		
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Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr				
20	25	30		
Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser				
35	40	45		
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr				
50	55	60		
Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe				
65	70	75	80	
Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu				
85	90	95		
Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala				

100	105	110
Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile		
115	120	125
Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg		
130	135	140
Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr		
145	150	160
Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala		
165	170	175
Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu		
180	185	190
Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp		
195	200	205

<210> 3
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 <212> DNA
 <213> Lawsonia intracellularis

<220>
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1	15
5	
10	
aca ttt tta cgt att agt gtt gtc tta ttt atg ctt cct ttt ttt tct	96
Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser	
20	30
25	
att gat ggt ttt cct aat atg tta aaa gca tca ata gct ctt att cta	144
Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu	
35	45
40	
act ata gtt ctt tgg ggg cgt ctt tct ctt tca gga aca caa atg cca	192
Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro	
50	60
55	
gcg cat cct ttc gat cta gta ttg tta atc ata agc gag gtt ttt ctt	240
Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu	
65	80
70	
75	
ggt att gta ttg ggg ctt gcg gta aac ttt ttc ttt gca gga att caa	288
Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Ala Gly Ile Gln	
85	95
90	
gct ggg gga gaa att ctt gct aca caa atg ggg ttt aca atg att acg	336
Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr	
100	110
105	
ctt gca gac cca tta act ggt aac acc aca ggt ttt att gca cat ttt	384
Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe	

115	120	125	
ctt tat atg gtt gct aca tta gtt ttt ctt gct ctt aat ggc cat ttg Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu 130	135	140	432
ttt ctt ata aaa gct ttt aca tat act ttt aaa atg gtt cca gca gga Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly 145	150	155	480
gga ctt gtt gta aga gaa att tta ttg agt gaa ctt ctt aat atg gca Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala 165	170	175	528
ggg atg att ttt gtt ttt gcc tta cat gtt gcg gca cca gtt atg tca Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser 180	185	190	576
gct ctt ttt tta gta gag atc tct tta gga ctt atg gca aga gct gct Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala 195	200	205	624
cct cag att cat att atg gaa gtt gga ttt cct gta aaa att ggt gta Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val 210	215	220	672
gga ttt ttc att gga cta tta ttt act atc tta tca aaa gaa acc Gly Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr 225	230	235	720
tat cga ttt att gca ggc cta gag gga cta ttt ttt aac tta ctt act Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr 245	250	255	768
gta atg ggt agt gga aaa tag Val Met Gly Ser Gly Lys 260			789

<210> 4
<211> 262
<212> PRT
<213> *Lawsonia intracellularis*

<400> 4			
Met Asn Leu Phe Asn Phe Asp Pro Ser Met Phe Leu Ser Phe Leu Leu			
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Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser			
20	25	30	
Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu			
35	40	45	
Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro			
50	55	60	
Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu			
65	70	75	80

Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Ala Gly Ile Gln
 85 90 95
 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
 100 105 110
 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
 115 120 125
 Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
 130 135 140
 Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
 145 150 155 160
 Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
 165 170 175
 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
 180 185 190
 Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
 195 200 205
 Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
 210 215 220
 Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
 225 230 235 240
 Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
 245 250 255
 Val Met Gly Ser Gly Lys
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<210> 5
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 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (1)...(1368)

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 1 5 10 15

 tca ttg aaa gga att ttt gaa gat gag ggc cat gaa gtt tta gaa aga 96
 Ser Leu Lys Gly Ile Phe Glu Asp Glu Gly His Glu Val Leu Glu Arg
 20 25 30

 gct tca gca gaa gga ctt aag tgt gtt gat gta gag tct cca gat 144
 Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp
 35 40 45

 ctt gtt ttt ctt gat att tgg ctt cct ggg atg gat ggt ctt atg gct 192
 Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
 50 55 60

 tta gac cat att cag gct ctt cat cag gaa tta cct gtt att atg att 240
 Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
 65 70 75 80

tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt	288
Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly	
85 90 95	
gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att	336
Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile	
100 105 110	
aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa	384
Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys	
115 120 125	
tta cta cgt act gta tta cct gag gag agt gag ttt ata gga cag tct	432
Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser	
130 135 140	
cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca	480
Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr	
145 150 155 160	
gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta	528
Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu	
165 170 175	
gct gca caa gca ttg cac aaa gga agc tca cga tat caa aaa cca ttt	576
Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe	
180 185 190	
ata gct gtt aat tgt gct gct atc cct gaa gaa ttg att gaa agc gaa	624
Ile Ala Val Asn Cys Ala Ala Pro Glu Glu Leu Ile Glu Ser Glu	
195 200 205	
cta ttt ggt cat gaa aaa ggg gcc ttt act ggt gcc gat gct tct cgt	672
Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg	
210 215 220	
gca ggt cgt ttt gag ttg gca cat aaa gga aca tta ttt ctt gat gaa	720
Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Phe Leu Asp Glu	
225 230 235 240	
ata gga gat atg agt tta aaa aca caa gca aaa att ttg cgt att ttg	768
Ile Gly Asp Met Ser Leu Lys Thr Gln Ala Lys Ile Leu Arg Ile Leu	
245 250 255	
caa gaa caa tgt ttt gaa aaa att ggt agt gtt aga act att aaa gtt	816
Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val	
260 265 270	
gat gta aga gtt att gca gca aca aat aag aat ctt gaa gac gct att	864
Asp Val Arg Val Ile Ala Ala Thr Asn Lys Asn Leu Glu Asp Ala Ile	
275 280 285	
agc gat gga aca ttt cgt caa gat ttg tat tat cgc tta cga gtt gtt	912
Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val	

290	295	300	
cca ttg cat ctt ccc cct ctt cgt gaa cgt gat tct gat att gag cta			960
Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu			
305	310	315	320
tta tta aat agg ttt gtg att cag ttg agt aaa cgt tat aga cgt gag			1008
Leu Leu Asn Arg Phe Val Ile Gln Leu Ser Lys Arg Tyr Arg Arg Glu			
325	330	335	
ccg cct att ttt tta gat gag gtc ttc cct gta ttg aaa caa tat tgt			1056
Pro Pro Ile Phe Leu Asp Glu Val Phe Pro Val Leu Lys Gln Tyr Cys			
340	345	350	
tgg cca ggg aat gta aga gaa tta ctt aat ttt gta gaa cga atg gtt			1104
Trp Pro Gly Asn Val Arg Glu Leu Leu Asn Phe Val Glu Arg Met Val			
355	360	365	
att ctt tat tca ggg aag aaa gta tgt ttg aca gat cct aag gta aaa			1152
Ile Leu Tyr Ser Gly Lys Lys Val Cys Leu Thr Asp Pro Lys Val Lys			
370	375	380	
agc aat tta aaa tat tta ccc aag aaa ttt tct tcc cat tat aac ttt			1200
Ser Asn Leu Lys Tyr Leu Pro Lys Phe Ser Ser His Tyr Asn Phe			
385	390	395	400
ctt ccc gat ata gat ttt aac cag gct aaa ata gct ttt gaa cca aaa			1248
Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys			
405	410	415	
ttt tta act gaa aaa tta cat gct tat caa gga aat att acc cga tta			1296
Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu			
420	425	430	
gca gaa gct att gga ctt gaa aga agt tat tta tat aga aag cta aaa			1344
Ala Glu Ala Ile Gly Leu Glu Arg Ser Tyr Leu Tyr Arg Lys Leu Lys			
435	440	445	
agc tat ggt att tat ctg tct gag tga			1371
Ser Tyr Gly Ile Tyr Leu Ser Glu			
450	455		
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<211> 456			
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<213> <i>Lawsonia intracellularis</i>			
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1	5	10	15
Ser Leu Lys Gly Ile Phe Glu Asp Glu Gly His Glu Val Leu Glu Arg			
20	25	30	
Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp			
35	40	45	

Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
 50 55 60
 Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
 65 70 75 80
 Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly
 85 90 95
 Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile
 100 105 110
 Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys
 115 120 125
 Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser
 130 135 140
 Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr
 145 150 155 160
 Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu
 165 170 175
 Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe
 180 185 190
 Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu
 195 200 205
 Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg
 210 215 220
 Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Phe Leu Asp Glu
 225 230 235 240
 Ile Gly Asp Met Ser Leu Lys Thr Gln Ala Lys Ile Leu Arg Ile Leu
 245 250 255
 Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val
 260 265 270
 Asp Val Arg Val Ile Ala Ala Thr Asn Lys Asn Leu Glu Asp Ala Ile
 275 280 285
 Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val
 290 295 300
 Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu
 305 310 315 320
 Leu Leu Asn Arg Phe Val Ile Gln Leu Ser Lys Arg Tyr Arg Arg Glu
 325 330 335
 Pro Pro Ile Phe Leu Asp Glu Val Phe Pro Val Leu Lys Gln Tyr Cys
 340 345 350
 Trp Pro Gly Asn Val Arg Glu Leu Leu Asn Phe Val Glu Arg Met Val
 355 360 365
 Ile Leu Tyr Ser Gly Lys Lys Val Cys Leu Thr Asp Pro Lys Val Lys
 370 375 380
 Ser Asn Leu Lys Tyr Leu Pro Lys Lys Phe Ser Ser His Tyr Asn Phe
 385 390 395 400
 Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys
 405 410 415
 Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu
 420 425 430
 Ala Glu Ala Ile Gly Leu Glu Arg Ser Tyr Leu Tyr Arg Lys Leu Lys
 435 440 445
 Ser Tyr Gly Ile Tyr Leu Ser Glu
 450 455

<211> 412
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (1)...(411)

<400> 7
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1 5 10 15

aat ctt caa gtc aat ttt tct aac cca tac cat caa aca gat att gaa 96
Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu
20 25 30

gtc ctg gct aat gca aaa aaa gtt aaa ggg atg aag ttt cca caa gac 144
Val Leu Ala Asn Ala Lys Lys Val Lys Gly Met Lys Phe Pro Gln Asp
35 40 45

ttt aat aaa cct gaa gtt ata gtt gct ata cgt aat ggt agt aca gtt 192
Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val
50 55 60

att act cct gca aag caa ctt ctt cct aaa gca tct ttt aga ctc ttt 240
Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe
65 70 75 80

gat gat gaa gtt gca tct ata aaa gat gta gaa tct gga caa tca cat 288
Asp Asp Glu Val Ala Ser Ile Lys Asp Val Glu Ser Gly Gln Ser His
85 90 95

ata tta tta gct tca gca cca tta cca gcg att caa gct ata aac tca 336
Ile Leu Leu Ala Ser Ala Pro Leu Pro Ala Ile Gln Ala Ile Asn Ser
100 105 110

aat ggc aac ctt att cgt tta gat aca ctc ccc att act cat caa tct 384
Asn Gly Asn Leu Ile Arg Leu Asp Thr Leu Pro Ile Thr His Gln Ser
115 120 125

gta gga ttt gca ata aag aag gga gat c 412
Val Gly Phe Ala Ile Lys Lys Gly Asp
130 135

<210> 8
<211> 137
<212> PRT
<213> Lawsonia intracellularis

<400> 8
Lys Gln Ile Asp Ile Ile Ser Gly Ala Thr Ile Thr Leu Glu Arg
1 5 10 15
Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu

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Val Leu Ala Asn Ala Lys Lys Val Lys Gly Met Lys Phe Pro Gln Asp			
35	40	45	
Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val			
50	55	60	
Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe			
65	70	75	80
Asp Asp Glu Val Ala Ser Ile Lys Asp Val Glu Ser Gly Gln Ser His			
85	90	95	
Ile Leu Leu Ala Ser Ala Pro Leu Pro Ala Ile Gln Ala Ile Asn Ser			
100	105	110	
Asn Gly Asn Leu Ile Arg Leu Asp Thr Leu Pro Ile Thr His Gln Ser			
115	120	125	
Val Gly Phe Ala Ile Lys Lys Gly Asp			
130	135		

<210> 9
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 <212> DNA
 <213> Lawsonia intracellularis

<220>
 <221> CDS
 <222> (1)...(846)

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1	5	10	15			
ggc tac ctt atg gct aaa ggg aat ctt gct tta ctc ttt caa cct gca						96
Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala						
20	25	30				
gaa ctt gtt atc att att ggg gca gca tta ggt gct ttt ttt gct tca						144
Glu Leu Val Ile Ile Ile Gly Ala Ala Leu Gly Ala Phe Phe Ala Ser						
35	40	45				
cag acg aaa tat tca ttt act ctg gtc att aaa aat tta tca cac att						192
Gln Thr Lys Tyr Ser Phe Thr Leu Val Ile Lys Asn Leu Ser His Ile						
50	55	60				
ttt ggc gat cca aac agt aca aaa ata aaa tac ctt gaa aca ctt gcc						240
Phe Gly Asp Pro Asn Ser Thr Lys Ile Lys Tyr Leu Glu Thr Leu Ala						
65	70	75	80			
ctt ctc tat gga ctt ttc tta aaa atg aat aga gaa ggt gtc att agt						288
Leu Leu Tyr Gly Leu Phe Leu Lys Met Asn Arg Glu Gly Val Ile Ser						
85	90	95				
ata gaa agt gat ata gaa aaa cct gaa tca agt cct atc ttt agt aaa						336
Ile Glu Ser Asp Ile Glu Lys Pro Glu Ser Ser Pro Ile Phe Ser Lys						
100	105	110				

tac cct aca att gta aaa gat act aaa gtt gtt gcc ttt att gca gat	384		
Tyr Pro Thr Ile Val Lys Asp Thr Lys Val Val Ala Phe Ile Ala Asp			
115	120	125	
aca tta cga gtt tat ctg aca aca ggt gca cca gaa gat ata gat aac	432		
Thr Leu Arg Val Tyr Leu Thr Thr Gly Ala Pro Glu Asp Ile Asp Asn			
130	135	140	
ctc atg gaa tct gac atg aaa att aca cac gaa gaa tta tta cct	480		
Leu Met Glu Ser Asp Met Lys Ile Thr His Glu Glu Glu Leu Leu Pro			
145	150	155	160
gca cat tcc atc agc cat atg gca gag tcg cta cca gga atg ggt att	528		
Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile			
165	170	175	
gtt gct gca gta tta ggt gtt gtt att acc atg gga aaa att aat gag	576		
Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu			
180	185	190	
cct cca gaa gtc ctt ggg cat tat att gga gca gct ttg gtt ggt aca	624		
Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr			
195	200	205	
ttt ata ggt att ctt ttc tgt tat ggt ttt ttt gga cct atg ggt tca	672		
Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser			
210	215	220	
aag ctt gaa acc tct gca gaa gaa gca cat ttt tat tat aat tcc att	720		
Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile			
225	230	235	240
aaa gaa gct gtt gca gct gct atc cga ggt tct aca cca atg ata gca	768		
Lys Glu Ala Val Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala			
245	250	255	
gta gaa tat gga aga cgt gcc ata cct aat aca ttt cgt cca tca ttt	816		
Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe			
260	265	270	
tcg gaa atg gaa gaa cgt cta aaa aca gga taa	849		
Ser Glu Met Glu Glu Arg Leu Lys Thr Gly			
275	280		

<210> 10
 <211> 282
 <212> PRT
 <213> *Lawsonia intracellularis*

<400> 10
 Met Tyr Ile Ile Ile Gly Tyr Phe Ile Val Ile Ala Ser Ile Ile Gly
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 Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala
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Glu	Leu	Val	Ile	Ile	Gly	Ala	Ala	Leu	Gly	Ala	Phe	Phe	Ala	Ser	
35					40					45					
Gln	Thr	Lys	Tyr	Ser	Phe	Thr	Leu	Val	Ile	Lys	Asn	Leu	Ser	His	Ile
50					55					60					
Phe	Gly	Asp	Pro	Asn	Ser	Thr	Lys	Ile	Lys	Tyr	Leu	Glu	Thr	Leu	Ala
65					70					75				80	
Leu	Leu	Tyr	Gly	Leu	Phe	Leu	Lys	Met	Asn	Arg	Glu	Gly	Val	Ile	Ser
														95	
85									90						
Ile	Glu	Ser	Asp	Ile	Glu	Lys	Pro	Glu	Ser	Ser	Pro	Ile	Phe	Ser	Lys
														110	
100									105						
Tyr	Pro	Thr	Ile	Val	Lys	Asp	Thr	Lys	Val	Val	Ala	Phe	Ile	Ala	Asp
														125	
115									120						
Thr	Leu	Arg	Val	Tyr	Leu	Thr	Thr	Gly	Ala	Pro	Glu	Asp	Ile	Asp	Asn
130								135				140			
Leu	Met	Glu	Ser	Asp	Met	Lys	Ile	Thr	His	Glu	Glu	Glu	Leu	Leu	Pro
														160	
145									150			155			
Ala	His	Ser	Ile	Ser	His	Met	Ala	Glu	Ser	Leu	Pro	Gly	Met	Gly	Ile
														175	
165										170					
Val	Ala	Ala	Val	Leu	Gly	Val	Val	Ile	Thr	Met	Gly	Lys	Ile	Asn	Glu
														190	
180										185					
Pro	Pro	Glu	Val	Leu	Gly	His	Tyr	Ile	Gly	Ala	Ala	Leu	Val	Gly	Thr
									195			200			205
195															
Phe	Ile	Gly	Ile	Leu	Phe	Cys	Tyr	Gly	Phe	Phe	Gly	Pro	Met	Gly	Ser
210								215				220			
Lys	Leu	Glu	Thr	Ser	Ala	Glu	Glu	Ala	His	Phe	Tyr	Tyr	Asn	Ser	Ile
														240	
225								230			235				
Lys	Glu	Ala	Val	Ala	Ala	Ala	Ile	Arg	Gly	Ser	Thr	Pro	Met	Ile	Ala
									245		250				255
245															
Val	Glu	Tyr	Gly	Arg	Arg	Ala	Ile	Pro	Asn	Thr	Phe	Arg	Pro	Ser	Phe
									260		265				270
Ser	Glu	Met	Glu	Glu	Arg	Leu	Lys	Thr	Gly						
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<212> DNA

<213> Lawsonia intracellularis

<220>

<221> CDS

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Met	Ser	Gly	Ser	Trp	Lys	Val	Ala	Tyr	Ala	Asp	Phe	Val	Thr	Ala	Met
1						5					10				15

atg	gct	ttc	ttt	cta	ctg	atg	tgg	att	ctt	gca	atg	aca	ccc	cct	gag
Met	Ala	Phe	Phe	Leu	Leu	Met	Trp	Ile	Leu	Ala	Met	Thr	Pro	Pro	Glu
									20		25			30	

gtt	aaa	gaa	ggt	ctt	gct	gca	tat	ttt	tct	tca	tct	gat	gct	aca	ttt
Val	Lys	Glu	Gly	Leu	Ala	Ala	Tyr	Phe	Ser	Ser	Ser	Asp	Ala	Thr	Phe
									35		40			45	

aaa aca cct .gat agt tcg cca atc tct aac aat cct ctt atc aac caa	192
Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln	
50 55 60	
ata gat aaa ctt gat act cga caa tta aaa att aat gaa aca gaa caa	240
Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln	
65 70 75 80	
tct cat tat gct ctt gct aat aaa tta aaa aaa atg tta atg gct gat	288
Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp	
85 90 95	
gct atc cca cag tca gca aca gga ata agt gct gac gat gtt ggt gta	336
Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val	
100 105 110	
tta tta cgt gta aat tct aat tcc acg ttt ttt cct ggt aca gca act	384
Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr	
115 120 125	
ctt aca ccc gaa ggg aaa aaa gtt atg gga act gtt tta gcc gtt ctc	432
Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu	
130 135 140	
cgt gaa tat aat ctt tac ctt gtg ata cgt ggc cat gct gat att ggt	480
Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly	
145 150 155 160	
gaa ata aca aaa ggc agc cct ttt gct tct aac tgg gaa ctt tca gga	528
Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly	
165 170 175	
gct cgt gca gct gca gct gca cag tat ctt gta gag cac ggg ata aag	576
Ala Arg Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys	
180 185 190	
gct tca cga att cgc tct gta gga tat gca gat aca aga cct cta gaa	624
Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu	
195 200 205	
cct agt tct cct gaa gga agt aca aaa aat cgt cgt ata gaa ttc tat	672
Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr	
210 215 220	
ttt cat cgg cca gaa gtt atg tct tat ggc gtt gta tat taa	714
Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr *	
225 230 235	
tag	717
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<211> 237	
<212> PRT	
<213> Lawsonia intracellularis	

<400> 12

Met Ser Gly Ser Trp Lys Val Ala Tyr Ala Asp Phe Val Thr Ala Met
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Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
20 25 30
Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
35 40 45
Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
50 55 60
Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
65 70 75 80
Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
85 90 95
Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
100 105 110
Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
115 120 125
Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
130 135 140
Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
145 150 155 160
Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
165 170 175
Ala Arg Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
180 185 190
Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
195 200 205
Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
210 215 220
Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr
225 230 235

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<212> DNA

<213> Lawsonia intracellularis

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1 5 10 15

tta tgc tca atg atg gaa gct gct ata tac tct atc cct att act tat 96
Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
20 25 30

att gaa cac ctt cgt gaa cag gga agc aaa aaa gga gaa aaa ctt tat 144
Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
35 40 45

tat tta cat .agt aat att gat cag cct att aca gcc gta tta ata ttg	192
Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu	
50 55 60	
aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct	240
Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala	
65 70 75 80	
aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc	288
Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu	
85 90 95	
acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt	336
Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly	
100 105 110	
gtt gct tac tct aaa cgt att gct ata att ctc ctt aat cct ctc tct	384
Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser	
115 120 125	
att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta	432
Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu	
130 135 140	
aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac	480
Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp	
145 150 155 160	
atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca	528
Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro	
165 170 175	
tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat	576
Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr	
180 185 190	
gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa	624
Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu	
195 200 205	
aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat	672
Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr	
210 215 220	
agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att	720
Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile	
225 230 235 240	
atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa	768
Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu	
245 250 255	
aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt	816
Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser	

260	265	270	
caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat			864
Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His			
275	280	285	
ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt tcc			912
Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser			
290	295	300	
tta gaa gat gta tta gaa act atg ctt gga aga gaa att gtt gat gaa			960
Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu			
305	310	315	320
agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt			1008
Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser			
325	330	335	
gca tta atc caa aat aat aaa aat act ctt tta aaa taa			1047
Ala Leu Ile Gln Asn Asn Lys Asn Thr Leu Leu Lys			
340	345		
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20	25	30	
Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr			
35	40	45	
Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu			
50	55	60	
Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala			
65	70	75	80
Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu			
85	90	95	
Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly			
100	105	110	
Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser			
115	120	125	
Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu			
130	135	140	
Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp			
145	150	155	160
Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro			
165	170	175	
Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr			
180	185	190	
Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu			
195	200	205	

Asn	Leu	Thr	Val	Ser	Glu	Ala	Tyr	Ser	Asn	Pro	Lys	Ile	Trp	Asn	Tyr
210				215							220				
Ser	Arg	Ile	Pro	Thr	Tyr	Gly	Glu	Asn	Asn	Glu	Asp	Ile	Thr	Gly	Ile
225				230						235				240	
Ile	Gln	Arg	Tyr	Glu	Ile	Gly	Arg	Tyr	Met	Thr	Asn	Gly	Glu	Thr	Glu
					245				250				255		
Lys	Lys	Leu	Leu	Glu	Ile	Met	Gln	Pro	Ala	Lys	Phe	Val	Leu	Glu	Ser
					260				265			270			
Gln	Thr	Val	Asp	His	Leu	Leu	Leu	Ala	Phe	Leu	Glu	Glu	Arg	Gln	His
					275				280			285			
Leu	Phe	Ile	Val	Leu	Asp	Glu	Tyr	Gly	Gly	Leu	Ser	Gly	Val	Val	Ser
					290				295			300			
Leu	Glu	Asp	Val	Leu	Glu	Thr	Met	Leu	Gly	Arg	Glu	Ile	Val	Asp	Glu
305					310					315				320	
Ser	Asp	Thr	Thr	Pro	Asp	Leu	Arg	Ala	Leu	Ala	Lys	Lys	Arg	His	Ser
					325					330			335		
Ala	Leu	Ile	Gln	Asn	Asn	Lys	Asn	Thr	Leu	Leu	Lys				
					340					345					

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1				5					10				15			
ata	aca	gaa	aat	tat	ctc	ttt	gct	aca	tca	att	acc	act	tcc	aca	att	96
Ile	Thr	Glu	Asn	Tyr	Leu	Phe	Ala	Thr	Ser	Ile	Thr	Thr	Ser	Thr	Ile	
					20				25				30			
aac	caa	caa	cat	ata	gca	tat	aca	gtt	act	ttt	acc	tct	cca	gaa	aat	144
Asn	Gln	Gln	His	Ile	Ala	Tyr	Thr	Val	Thr	Phe	Thr	Ser	Pro	Glu	Asn	
					35				40			45				
cct	aat	ctt	gca	aca	gag	atg	gaa	aca	cat	agt	gaa	tta	gta	aag	ctt	192
Pro	Asn	Leu	Ala	Thr	Glu	Met	Glu	Thr	His	Ser	Glu	Leu	Val	Lys	Leu	
					50				55			60				
gca	aat	caa	tct	tta	gat	agt	aaa	ata	ggt	tta	aat	tta	cgt	gtt	aaa	240
Ala	Asn	Gln	Ser	Leu	Asp	Ser	Lys	Ile	Gly	Leu	Asn	Leu	Arg	Val	Lys	
					65				70			75		80		
gaa	gat	ata	agt	aca	gca	caa	aaa	att	ctt	gac	tcg	aat	ggt	tat	tat	288
Glu	Asp	Ile	Ser	Thr	Ala	Gln	Lys	Ile	Leu	Asp	Ser	Asn	Gly	Tyr	Tyr	
					85				90			95				
agt	gga	agt	gtc	gag	gga	aag	att	gac	tgg	cag	acg	aac	cct	att	agt	336

' Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser			
100	105	110	
atc caa atc caa ttt aaa cca aat gta caa tat aaa ata aat aca ata			384
Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile			
115	120	125	
cat atc caa tac ctt gat agt gaa ctt gca tat ctc cct ctt tcc tta			432
His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu			
130	135	140	
gaa gaa ttc aat ctc tct aaa ggt aat cct gct ctt gct gtt aat atc			480
Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile			
145	150	155	160
cta tcc tct gta agt agc ctc atg caa tat ata cat aat aat gga tat			528
Leu Ser Ser Val Sér Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr			
165	170	175	
cca tta gcc aaa ata aaa aaa act caa tac ata att aat cgg atg gat			576
Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp			
180	185	190	
tat aca ttt gat att gat tta gta ata aga caa gga ccg tta ctc cat			624
Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His			
195	200	205	
atg ggt aaa gta caa cct caa cat aat ctc aat att tca aca ata ttc			672
Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe			
210	215	220	
cta aat aaa att gct aca tgg aag gaa gga agg gta tgg aac aat gca			720
Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala			
225	230	235	240
ctc ctt gat tct tat cga aca cgg ctt caa caa aca ggc ctt ttc agt			768
Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser			
245	250	255	
tct ata act ctc aat cca agg aat caa aaa gaa caa aat ggt aac acc			816
Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr			
260	265	270	
tct ata gaa ctt gtt gca aca gaa gcc cct cca agg act att agt ggt			864
Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly			
275	280	285	
ggc tta caa tac tct gat caa ggt att ggt gca cgt ggg act tgg			912
Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp			
290	295	300	
gaa cat cga aat gtt ttt ggt aat gga gaa ctt ttt cgt ata aca gca			960
Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala			
305	310	315	320

cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca	325	330	335	1008
Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro				
gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa	340	345	350	1056
Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys				
aaa gaa aat aca aaa agt tac aaa caa caa ctt gca tct att gct tta	355	360	365	1104
Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu				
gga att gaa cga caa ttt aat aga cgt tgg ttt ggt agt agc agt ctt	370	375	380	1152
Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu				
tca gtt gat aca gga ttt atg gat gat cga gat tct ata aaa aaa ata	385	390	395	1200
Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile				
ttt act ctt ttt ggc atc ccc tta tca ata aca agg gat agt tct aaa	405	410	415	1248
Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys				
gat cct ctt aat cct atc caa gga aca aaa gct acc tta aat gtt act	420	425	430	1296
Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr				
cct tat att ggt aaa tat aaa aaa aag att ttg act tta cgt agt cgg	435	440	445	1344
Pro Tyr Ile Gly Lys Tyr Lys Lys Ile Leu Thr Leu Arg Ser Arg				
ttt gat ttt agc ttt tac ata gac gtt ctt aaa aca ggg aaa ctt atc	450	455	460	1392
Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile				
ttg gct aac aaa ata gca ata ggt tcc ctc cta ggg aaa gat ata gaa	465	470	475	1440
Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu				
aac tat cct gca ata cta agg ttt tat gct ggg ggt ggt agt gta	485	490	495	1488
Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Ser Val				
aga ggg tat gac tat caa tca ttg gga cca aaa aat aaa tat ggg gat	500	505	510	1536
Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp				
gct att gga gga ctt tct ttt tca act att agt ttt gaa tta cga tta	515	520	525	1584
Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu				
aaa ata aca gaa tcc att ggc att gtg cca att tat tgg atg ggg gaa	530	535	540	1632
Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu				

tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg	1680
Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Ser Ile Tyr Trp	
545 550 555 560	
ggg gta ggc ctg ggg cta cga tat tat aca agt ttt gcc ccc ata cgt	1728
Gly Val Gly Leu Gly Leu Arg Tyr Tyr Thr Ser Phe Ala Pro Ile Arg	
565 570 575	
tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt	1776
Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe	
580 585 590	
caa ctt tat att agt att ggg caa gca ttc taa tga	1812
Gln Leu Tyr Ile Ser Ile Gly Gln Ala Phe *	
595 600	

<210> 16
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Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn	
35 40 45	
Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu	
50 55 60	
Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys	
65 70 75 80	
Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr	
85 90 95	
Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser	
100 105 110	
Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile	
115 120 125	
His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu	
130 135 140	
Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile	
145 150 155 160	
Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr	
165 170 175	
Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp	
180 185 190	
Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His	
195 200 205	
Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe	
210 215 220	
Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala	
225 230 235 240	
Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser	

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Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr		
260	265	270
Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly		
275	280	285
Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp		
290	295	300
Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala		
305	310	315
320		
Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro		
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Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys		
340	345	350
Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu		
355	360	365
Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu		
370	375	380
Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile		
385	390	395
400		
Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys		
405	410	415
Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr		
420	425	430
Pro Tyr Ile Gly Lys Tyr Lys Lys Ile Leu Thr Leu Arg Ser Arg		
435	440	445
Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile		
450	455	460
Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu		
465	470	475
480		
Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Ser Val		
485	490	495
Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp		
500	505	510
Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu		
515	520	525
Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu		
530	535	540
Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp		
545	550	555
560		
Gly Val Gly Leu Gly Leu Arg Tyr Tyr Thr Ser Phe Ala Pro Ile Arg		
565	570	575
Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe		
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1 5 10 15	
gca ttt acg tta ttt tta gga ctt att att aca ggc att ctt ttt ata	96
Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile	
20 25 30	
cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta	144
Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu	
35 40 45	
ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca	192
Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro	
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Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn	
65 70 75 80	
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Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp	
85 90 95	
gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat	336
Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp	
100 105 110	
ctt gta tta tat cgc tta ccc tca aat aat aat cta aaa aaa tca tct	384
Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser	
115 120 125	
aca agt ttt gtg tta cct cac ata tca ttt gat tta act cca tgg tgg	432
Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp	
130 135 140	
act gaa cat att cgt att caa aac atc cat att aac aat aca caa ctt	480
Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu	
145 150 155 160	
tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat	528
Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp	
165 170 175	
ggt aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac	576
Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn	
180 185 190	
aaa aca aaa att ata gga acg ctt cgt tac caa ggg aat aag aca caa	624
Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln	
195 200 205	
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Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp			
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Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro			
225	230	235	240
ctc cat tta cac ctt tct att tat cct gaa cat aat aga att atc tta			768
Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu			
245	250	255	
cac tca tta cta gct gaa tat ggt agc tgg tta ctt aca tca gaa agt			816
His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser			
260	265	270	
att gaa gta tct aat gag caa tta aaa gga aat att tta tta aaa tat			864
Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr			
275	280	285	
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Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser			
290	295	300	
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Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met			
305	310	315	320
aca tta cct gaa att aac att aca aaa aac ata ata gat ctt caa aca			1008
Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr			
325	330	335	
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Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu			
340	345	350	
aca tct ggg aca att aca gta cag gga gaa act ata ccc aat agt att			1104
Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile			
355	360	365	
ctt tcc agt gca gtt gat ata ata gcc tct aca aca aca cat aca att			1152
Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr His Thr Ile			
370	375	380	
acc tta gag cat gca acc tta aca tct cca gaa atg cat ttt tcc cta			1200
Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu			
385	390	395	400
tct gga gaa ttt aat agt ctt cta gga aat atc gat gca aac cta aaa			1248
Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys			
405	410	415	
ggc aat act cca act ctt agt ata ttt tct tct ctt ctt gga cta cct			1296
Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro			
420	425	430	

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aac tgg gga gta caa gca tta cag ggg aca tta ggt gat aat gca act Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr 465 470 475 480	1440
cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu 485 490 495	1488
aac aaa ttg aaa tta aca gca aag aat gtt tat gct gaa ggc ctt att Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile 500 505 510	1536
aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro 515 520 525	1584
aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu 530 535 540	1632
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ctc ata ata act act caa tct tct tcc tct gcg att aaa ggt aat Leu Ile Ile Thr Thr Gln Ser Ser Ser Ala Ile Lys Gly Asn 580 585 590	1776
ata aca ctc tcg gct gag cca gct tca tct gag gca tta acc ttt tca Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser 595 600 605	1824
agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile 610 615 620	1872
gga aat ata tta gga gta aat ctt gat ggt aat att aaa ata aca aaa Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys 625 630 635 640	1920
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ata aaa ata cag ttt gat cca aag aat caa caa tgt att tct act caa Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln 675 680 685	2064
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ata aaa gga aga gca gat aca ata caa ctt cat aag aat cct aca att Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile 705 710 715 720	2160
gct ctc tct tca aaa att ggt gct ggt aca tat gaa gac ttt caa tgg Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp 725 730 735	2208
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aaa ata aat ata gca gga caa aca act gta aac gca aac ttt caa aca Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr 755 760 765	2304
aat ctt ttt gaa aaa aat att aat ata act act ctt aat tta aaa aat Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn 770 775 780	2352
att caa aaa aat ata gga att aag ctc ctt cag cca ata aaa att ata Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile 785 790 795 800	2400
gtc tca cct caa caa ttt gtt ctt aat aac tgt tca cta gca att ctt Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu 805 810 815	2448
cca tct gga aca att aca act gat ata tat gtt act cct caa cga ctt Pro Ser Gly Thr Ile Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu 820 825 830	2496
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865	870	875	880	
aac ata cat tat cca agg cca aat cca tca ata gca aac tta cat gta				2688
Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val				
885	890	895		
gaa ggg gaa att ata tct tct cct aac aat ata tgt aaa ctt aat gca				2736
Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala				
900	905	910		
acc cta aca gaa aaa aaa gag cct ata cct ata tca ata caa gca aca				2784
Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ile Ser Ile Gln Ala Thr				
915	920	925		
ctc cct ttt gag ttc aca gaa aac aat atc cct atg cta tct aaa atg				2832
Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met				
930	935	940		
agg cct ttt tct gcc cat atc aag tgg act gga ata tta gat aca ctt				2880
Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu				
945	950	955	960	
tgg aaa ctc att cca ctt act gat tac att atg gct ggg aat gga tct				2928
Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser				
965	970	975		
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Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile				
980	985	990		
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Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu				
995	1000	1005		
tac tta gaa aat atc aat gct aaa tta cag gtc ttt tct aat aga atc				3072
Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile				
1010	1015	1020		
tcc cat att caa gct aca gca tct gat ggt aaa caa ggt agt ata caa				3120
Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln				
1025	1030	1035	1040	
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Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile				
1045	1050	1055		
aat ggc tcc ttt aca aac ctt gct cca tta caa cgt aaa gac cta agt				3216
Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser				
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ctt aca ctt tca gga gca gct act ctt gaa gga aca tta aaa cag tct				3264
Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser				
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Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr			
1090	1095	1100	
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Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr			
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caa caa caa aat aca aag acc aaa aaa gct acc tat caa caa cct acc	3408		
Gln Gln Gln Asn Thr Lys Thr Lys Ala Thr Tyr Gln Gln Pro Thr			
1125	1130	1135	
tta tct att gcg tta agt atc ccg aat cgt ttt ttt gtc cgt agt agt	3456		
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1140	1145	1150	
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Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile			
1155	1160	1165	
aca agt cct gtt att aca gga gca cta act tct ata aga gga aat ttt	3552		
Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe			
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Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe			
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Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr			
1205	1210	1215	
tca tca cct tct att aca gct ata ggc att att aaa ggt aca act agt	3696		
Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser			
1220	1225	1230	
aat cct aat att act ttt tca agt aca cca cct tta cct caa gat gaa	3744		
Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu			
1235	1240	1245	
ata gtt tcc caa gtt ctt ttt ggt aaa agc tca caa agt ctt agc agg	3792		
Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg			
1250	1255	1260	
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Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe			
1265	1270	1275	1280
aat act gga agt atg aat ttc cta aca aat att cga cag aca tta ggg	3888		
Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly			
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Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr			
1300	1305	1310	

tcc aac tca aac gat caa ata gaa gat atc cct gtt ata gaa cta ggt			3984
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Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu			
1330	1335	1340	
gat agt aat gat act ggg gca aga ata tca gtt gaa ctt gca cct aat			4080
Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn			
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ttt aat ctt gaa ggt aga aca ggg act caa tat agt gag ata ggt att			4128
Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile			
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Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu			
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Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro			
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Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn			
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Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp			
85	90	95	
Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp			
100	105	110	
Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Leu Lys Lys Ser Ser			
115	120	125	
Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp			
130	135	140	
Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu			
145	150	155	160
Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp			
165	170	175	
Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Asn			
180	185	190	
Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln			
195	200	205	
Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp			
210	215	220	

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 Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu
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 His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser
 260 265 270
 Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr
 275 280 285
 Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser
 290 295 300
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 Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr
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 Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu
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 355 360 365
 Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr His Thr Ile
 370 375 380
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 Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
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 Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
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 Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
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 450 455 460
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 Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu
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 580 585 590
 Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
 595 600 605
 Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
 610 615 620
 Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys
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 Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp
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 Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser

660	665	670
Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln		
675	680	685
Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr		
690	695	700
Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile		
705	710	715
Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp		
725	730	735
Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser		
740	745	750
Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr		
755	760	765
Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn		
770	775	780
Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile		
785	790	795
Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu		
805	810	815
Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu		
820	825	830
Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro		
835	840	845
Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu		
850	855	860
Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu		
865	870	875
Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val		
885	890	895
Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala		
900	905	910
Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ser Ile Gln Ala Thr		
915	920	925
Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met		
930	935	940
Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu		
945	950	955
Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser		
965	970	975
Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile		
980	985	990
Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu		
995	1000	1005
Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile		
1010	1015	1020
Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln		
1025	1030	1035
Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile		
1045	1050	1055
Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser		
1060	1065	1070
Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser		
1075	1080	1085
Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr		
1090	1095	1100

Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr
 1105 1110 1115 1120
 Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr
 1125 1130 1135
 Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser
 1140 1145 1150
 Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile
 1155 1160 1165
 Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe
 1170 1175 1180
 Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe
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 Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr
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 Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser
 1220 1225 1230
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 1250 1255 1260
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 1315 1320 1325
 Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
 1330 1335 1340
 Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
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Gly Ser
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His His His His His

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